

**[00065]** This invention provides a method for rapidly obtaining accurate three-dimensional structure of proteins including large or multi-sub unit proteins, using a combination of NMR analysis of backbone only  $^{13}\text{C}$ ,  $^{15}\text{N}$  or  $^{13}\text{C}$  and  $^{15}\text{N}$  isotopically labeled proteins which are optionally also  $^2\text{H}$  isotopically labeled in the  $\text{C}\alpha$  position protons and residual dipolar coupling measurements in more than one partially aligned state.

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